

SEQUENCE LISTING

<110> Keating, Mark T.
Splawski, Igor

<120> MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT SYNDROME GENE

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<150> US 09/735,995
<151> 2000-12-14

<150> US 09/226,012
<151> 1999-01-06

<150> US 09/122,847
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<170> PatentIn Ver. 2.0

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Ser Pro Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His	
240 245 250	
agc ctc aac ccc gac gcc tcg ggc tcc agc tgc agc ctg gcc cgg acg	876
Ser Leu Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr	
255 260 265 270	
cgc tcc cga gaa agc tgc gcc agc gtg cgc cgc gcc tcg tcg gcc gac	924
Arg Ser Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp	
275 280 285	
gac atc gag gcc atg cgc gcc ggg gtg ctg ccc ccg cca ccg cgc cac	972
Asp Ile Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Arg His	

290	295	300	
gcc agc acc ggg gcc atg cac cca ctg cgc agc ggc ttg ctc aac tcc Ala Ser Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser 305	310	315	1020
acc tcg gac tcc gac ctc gtg cgc tac cgc acc att agc aag att ccc Thr Ser Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro 320	325	330	1068
caa atc acc ctc aac ttt gtg gac ctc aag ggc gac ccc ttc ttg gct Gln Ile Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala 335	340	345	1116
tcg ccc acc agt gac cgt gag atc ata gca cct aag ata aag gag cga Ser Pro Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg 355	360	365	1164
acc cac aat gtc act gag aag gtc acc cag gtc ctg tcc ctg ggc gcc Thr His Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala 370	375	380	1212
gac gtg ctg cct gag tac aag ctg cag gca ccg cgc atc cac cgc tgg Asp Val Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp 385	390	395	1260
acc atc ctg cat tac agc ccc ttc aag gcc gtg tgg gac tgg ctc atc Thr Ile Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile 400	405	410	1308
ctg ctg ctg gtc atc tac acg gct gtc ttc aca ccc tac tcg gct gcc Leu Leu Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala 415	420	425	1356
ttc ctg ctg aag gag acg gaa gaa ggc ccg cct gct acc gag tgt ggc Phe Leu Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly 435	440	445	1404
tac gcc tgc cag ccg ctg gct gtg gtg gac ctc atc gtg gac atc atg Tyr Ala Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met 450	455	460	1452
ttc att gtg gac atc ctc atc aac ttc cgc acc acc tac gtc aat gcc Phe Ile Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala 465	470	475	1500
aac gag gag gtg gtc agc cac ccc ggc cgc atc gcc gtc cac tac ttc Asn Glu Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe 480	485	490	1548
aag ggc tgg ttc ctc atc gac atg gtg gcc atc ccc ttc gac ctg Lys Gly Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu 495	500	505	1596
ctc atc ttc ggc tct ggc tct gag gag ctg atc ggg ctg ctg aag act Leu Ile Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr 515	520	525	1644
gcg cgg ctg ctg cgg ctg gtg cgc gtg gcg cgg aag ctg gat cgc tac Ala Arg Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr 530	535	540	1692
tca gag tac ggc gcg gcc gtg ctg ttc ttg ctc atg tgc acc ttt gcg Ser Glu Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala			1740

545	550	555	
ctc atc gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg Leu Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met 560 565 570			1788
gag cag cca cac atg gac tca cgc atc ggc tgg ctg cac aac ctg ggc Glu Gln Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly 575 580 585 590			1836
gac cag ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc Asp Gln Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser 595 600 605			1884
atc aag gac aag tat gtg acg gcg ctc tac ttc acc ttc agc agc ctc Ile Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu 610 615 620			1932
acc agt gtg ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag Thr Ser Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys 625 630 635			1980
atc ttc tcc atc tgc gtc atg ctc att ggc tcc ctc atg tat gct agc Ile Phe Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser 640 645 650			2028
atc ttc ggc aac gtg tcg gcc atc atc cag cgg ctg tac tcg ggc aca Ile Phe Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr 655 660 665 670			2076
gcc cgc tac cac aca cag atg ctg cgg gtg cgg gag ttc atc cgc ttc Ala Arg Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe 675 680 685			2124
cac cag atc ccc aat ccc ctg cgc cag cgc ctc gag gag tac ttc cag His Gln Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln 690 695 700			2172
cac gcc tgg tcc tac acc aac ggc atc gac atg aac gcg gtg ctg aag His Ala Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys 705 710 715			2220
ggc ttc cct gag tgc ctg cag gct gac atc tgc ctg cac ctg aac cgc Gly Phe Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg 720 725 730			2268
tca ctg ctg cag cac tgc aaa ccc ttc cga ggg gcc acc aag ggc tgc Ser Leu Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys 735 740 745 750			2316
ctt cgg gcc ctg gcc atg aag ttc aag acc aca cat gca ccc cca ggg Leu Arg Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly 755 760 765			2364
gac aca ctg gtg cat gct ggg gac ctg ctc acc gcc ctg tac ttc atc Asp Thr Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile 770 775 780			2412
tcc cgg ggc tcc atc gag atc ctg cgg ggc gac gtc gtc gtg gcc atc Ser Arg Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile 785 790 795			2460
ctg ggg aag aat gac atc ttt ggg gag cct ctg aac ctg tat gca agg Leu Gly Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg			2508

800	805	810	
cct ggc aag tcg aac ggg gat gtg cg ^g gcc ctc acc tac tgt gac cta Pro Gly Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu 815 820 825 830			2556
cac aag atc cat cg ^g gac gac ctg ctg gag gtg ctg gac atg tac cct His Lys Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro 835 840 845			2604
gag ttc tcc gac cac ttc tgg tcc agc ctg gag atc acc ttc aac ctg Glu Phe Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu 850 855 860			2652
cga gat acc aac atg atc ccg ggc tcc ccc ggc agt acg gag tta gag Arg Asp Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu 865 870 875			2700
ggt ggc ttc agt cg ^g caa cg ^c aag cg ^c aag ttg tcc ttc cg ^c agg cg ^c Gly Gly Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg 880 885 890			2748
acg gac aag gac acg gag cag cca ggg gag gtg tcg gcc ttg ggg ccg Thr Asp Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro 895 900 905 910			2796
ggc cg ^g gc ^g ggg gca ggg ccg agt agc cg ^g ggc cg ^g ccg ggg ggg ccg Gly Arg Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro 915 920 925			2844
tgg ggg gag agc ccg tcc agt ggc ccc tcc agc cct gag agc agt gag Trp Gly Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu 930 935 940			2892
gat gag ggc cca ggc cg ^c agc tcc agc ccc ctc cg ^c ctg gtg ccc ttc Asp Glu Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe 945 950 955			2940
tcc agc ccc agg ccc ccc gga gag ccg ccg ggt ggg gag ccc ctg atg Ser Ser Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met 960 965 970			2988
gag gac tgc gag aag agc agc gac act tgc aac ccc ctg tca ggc gcc Glu Asp Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala 975 980 985 990			3036
ttc tca gga gtg tcc aac att ttc agc ttc tgg ggg gag agt cg ^g ggc Phe Ser Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly 995 1000 1005			3084
cg ^c cag tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc Arg Gln Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu 1010 1015 1020			3132
ctc aac atc ccc ctc tcc agc ccg ggt cg ^g cg ^g ccc ccg ggc gac gtg Leu Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val 1025 1030 1035			3180
gag agc agg ctg gat gcc ctc cag cg ^c cag ctc aac agg ctg gag acc Glu Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr 1040 1045 1050			3228
cg ^g ctg agt gca gac atg gcc act gtc ctg cag ctg cta cag agg cag Arg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln			3276

1055	1060	1065	1070	
atg acg ctg gtc ccg ccc gcc tac agt gct gtg acc acc ccg ggg cct Met Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro				3324
1075	1080		1085	
ggc ccc act tcc aca tcc ccg ctg ttg ccc gtc agc ccc ctc ccc acc Gly Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr				3372
1090	1095		1100	
ctc acc ttg gac tcg ctt tct cag gtt tcc cag ttc atg gcg tgt gag Leu Thr Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu				3420
1105	1110		1115	
gag ctg ccc ccg ggg gcc cca gag ctt ccc caa gaa ggc ccc aca cga Glu Leu Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg				3468
1120	1125		1130	
cgc ctc tcc cta ccg ggc cag ctg ggg gcc ctc acc tcc cag ccc ctg Arg Leu Ser Leu Pro Gly Gln Leu Gly Ala Leu Thr Ser Gln Pro Leu				3516
1135	1140		1145	
cac aga cac ggc tcg gac ccg ggc agt tagtggggct gcccagtgtg His Arg His Gly Ser Asp Pro Gly Ser				3563
1155				
gacacgtggc tcacccaggg atcaaggcgc tgctgggccc ctccccttgg aggccctgct				3623
caggaggccc tgaccgtgga aggggagagg aactcgaaag cacagctcct ccccccagccc				3683
ttgggaccat cttctcctgc agtcccctgg gccccagtga gaggggcagg ggcagggccg				3743
gcagtaggtg gggcctgtgg tccccccact gcccctgaggg cattagctgg tctaactgcc				3803
cgaggaggcacc cggccctggg ccttaggcac ctcaaggact tttctgctat ttactgctct				3863
tattgttaag gataataatt aaggatcata tgaataatta atgaagatgc tgatgactat				3923
gaataataaa taattatcct gaggaga				3950

<210> 4
 <211> 1159
 <212> PRT
 <213> Homo sapiens

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Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu Asp				
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Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile Ala				
20	25		30	
Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe				
35	40		45	
Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys				
50	55		60	
Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala				
65	70		75	
Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile				
85	90		95	

Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val
 100 105 110
 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn
 115 120 125
 Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp
 130 135 140
 Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala
 145 150 155 160
 Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg
 165 170 175
 Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro Gly
 180 185 190
 Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser Glu
 195 200 205
 Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala Gly
 210 215 220
 Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser Pro
 225 230 235 240
 Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser Leu
 245 250 255
 Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg Ser
 260 265 270
 Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp Ile
 275 280 285
 Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Arg His Ala Ser
 290 295 300
 Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr Ser
 305 310 315 320
 Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile
 325 330 335
 Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro
 340 345 350
 Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His
 355 360 365
 Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val
 370 375 380
 Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr Ile
 385 390 395 400
 Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu
 405 410 415
 Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe Leu
 420 425 430
 Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr Ala

435	440	445	
Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe Ile			
450	455	460	
Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn Glu			
465	470	475	480
Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys Gly			
485	490	495	
Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile			
500	505	510	
Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala Arg			
515	520	525	
Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu			
530	535	540	
Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile			
545	550	555	560
Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu Gln			
565	570	575	
Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp Gln			
580	585	590	
Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile Lys			
595	600	605	
Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser			
610	615	620	
Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile Phe			
625	630	635	640
Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe			
645	650	655	
Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg			
660	665	670	
Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His Gln			
675	680	685	
Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala			
690	695	700	
Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe			
705	710	715	720
Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg Ser Leu			
725	730	735	
Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu Arg			
740	745	750	
Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr			
755	760	765	
Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser Arg			
770	775	780	

Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu Gly
 785 790 795 800

Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro Gly
 805 810 815

Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys
 820 825 830

Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu Phe
 835 840 845

Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg Asp
 850 855 860

Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly Gly
 865 870 875 880

Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr Asp
 885 890 895

Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly Arg
 900 905 910

Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp Gly
 915 920 925

Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu
 930 935 940

Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser
 945 950 955 960

Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp
 965 970 975

Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser
 980 985 990

Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln
 995 1000 1005

Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu Asn
 1010 1015 1020

Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val Glu Ser
 1025 1030 1035 1040

Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr Arg Leu
 1045 1050 1055

Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln Met Thr
 1060 1065 1070

Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro Gly Pro
 1075 1080 1085

Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr Leu Thr
 1090 1095 1100

Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu Glu Leu
 1105 1110 1115 1120

Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg Arg Leu

1125

1130

1135

Ser Leu Pro Gly Gln Leu Gly Ala Leu Thr Ser Gln Pro Leu His Arg
 1140 1145 1150

His Gly Ser Asp Pro Gly Ser
 1155

<210> 5
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hypothetical
 sequence for the example of calculating homology.

<400> 5
 accgttagcta cgtacgtata tagaaagggc gcgatcgctcg tcgcgtatga cgacttagca 60
 tgc 63

<210> 6
 <211> 130
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hypothetical
 sequence for example of calculating homology.

<400> 6
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 cgggatcgctc cgtcgcgtat gacgacttag ccatgcacgg tatatcgat taggactagc 120
 gattgacttag 130

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 <211> 20
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<400> 7
 gctggggccgc tccccttgaa 20

<210> 8
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<400> 8
 gcatcttcat taattattca 20

<210> 9
 <211> 20
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<400> 9
gacgtgctgc ctgagttacaa

20

<210> 10
<211> 22
<212> DNA
<213> Homo sapiens

<400> 10
ttcctgctga aggagacgga ag

22

<210> 11
<211> 21
<212> DNA
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<400> 11
accacctacg tcaatgccaa c

21

<210> 12
<211> 21
<212> DNA
<213> Homo sapiens

<400> 12
tgcccccatac acggaatgtg c

21

<210> 13
<211> 19
<212> DNA
<213> Homo sapiens

<400> 13
gatcgctact cagagtacg

19

<210> 14
<211> 22
<212> DNA
<213> Homo sapiens

<400> 14
gcctgggcgg cccctccatc aa

22

<210> 15
<211> 21
<212> DNA
<213> Homo sapiens

<400> 15
cacctccctcg ttggcattga c

21

<210> 16
<211> 25
<212> DNA
<213> Homo sapiens

<400> 16

gtcgaagggg atggcggcca ccatg	25
<210> 17	
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<210> 21	
<211> 19	
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<210> 35		
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<400> 35		
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ctctgaggag gtggggtcag	20	
<210> 38		

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